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Disease Notes

First Report of *Sida micrantha mosaic virus* in *Phaseolus vulgaris* in Brazil

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Snap and common beans (*Phaseolus vulgaris* L.) are severely affected by *Bean golden mosaic virus* (BGMV) infection, so far the only begomovirus reported on these crops in Brazil (1). Samples of snap and common beans colonized by the whitefly *Bemisia tabaci* biotype B and displaying golden mosaic, chlorotic spots, and leaf distortion were collected in three production regions in Goiás State (Goianópolis, Luziânia, and Itaberaí) between 2003 and 2007. Total DNA extracted from leaf samples was used as template in PCR assays using universal primers targeting conserved regions of the DNA-A and DNA-B genomes (3). Begomovirus-specific amplicons were observed only with DNA template from symptomatic plants. Two single amplicons were observed for both genomic segments, indicating the presence of bipartite species in all samples. Sequence analysis of four isolates (named as GO-176, GO-260, GO-354, and GO-368) obtained from common bean samples indicated identity levels of approximately 95% with the DNA-A segment of BGMV (GenBank Accession No. FJ665283). However, the complete DNA-A sequence (GenBank Accession No. HM357459.1) of the GO-060 isolate (from a symptomatic snap bean plant collected in Goianópolis) displayed 76% identity with BGMV (GenBank Accession No. FJ665283) and 95% identity with the DNA-A of a *Sida micrantha mosaic virus* (SimMV) isolate (GenBank Accession No. EU908733.1) reported to be infecting okra (*Abelmoschus esculentus* L.) and 94.8% with a SimMV isolate reported to be infecting soybean (GenBank Accession No. FJ686693) in Brazil (2). Koch's postulates were fulfilled for the isolate GO-060 by inoculating a set of soybean and bean accessions via a biolistic approach. The ratio of positive PCR amplicons per total of inoculated plants were 15 of 16 for snap bean cv. Trepador, 9 of 10 for snap bean cv. Fatura, 18 of 24 for common bean cv. Olate Pinto, and 19 of 25 for common bean cv. Carioca. The isolate was also able to infect eight of nine soybean 'Doko' plants. Sequence analysis using symptomatic leaf samples (15 days after inoculation) confirmed SimMV as the causal agent. To our knowledge, this is the first report of a SimMV isolate infecting *P. vulgaris*. This virus is apparently fast expanding its host range from Malvaceae to Solanaceae species and leguminous hosts after the introduction of *B. tabaci* biotype B (2). More extensive surveys are necessary to assess the current epidemiological importance of SimMV in both snap and common beans in Brazil.

References: (1) J.C. Faria and D. P. Maxwell. *Phytopathology* 89:262, 1999. (2) F. R. Fernandes et al. *Arch. Virol.* 154:1567, 2009. (3) M. R. Rojas et al. *Plant Dis.* 77:340, 1993.